```
NOV20:
                   CCRYPLTVDFEAFGWD-WIIAPKRYKANYCSGQCEYMFMQKYPHTH-----LVQQANPR
                   11
       Sbjct: 1
                   CRRHDLYVDFKDLGWDDWIIAPKGYNAYYCEGECPFPLSERLNATNHAIVQSLVHALDPG
             304 GSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS 345
      NOV20:
                      ||| |||+||++|||++|
                                        ++
                                             | | | | | + | | | |
      Sbjct:
             61
                  AVPKPCCVPTKLSPLSMLYYDDDGNVVLRNYPNMVVEECGCR
                                                          102 (SEQ ID NO:300)
      gnl|Pfam|pfam00019, TGF-beta, Transforming growth factor beta like domain.
                  CD-Length = 105 residues, 97.1% aligned
                  Score = 103 bits (256), Expect = 2e-23
      NOV20: 251 CCRYPLTVDFEAFGW-DWIIAPKRYKANYCSGQCEYMFMQKYPHTH-----LVQQANPR 303
                       1]+ [][
      Sbjct: 4
                  CRLRSLYVDFRDLGWGDWIIAPEGYIANYCSGSCPFPLRDDLNLSNHAILQTLVRLRNPR
            304 GSAGPCCTPTKMSPINMLYFNDKQQIIYGKIPGMVVDRCGCS
      NOV20:
                                                         345 (SEO ID NO:299)
                      ++
                                              1 1 1 111
      Sbjct: 64
                  {\tt AVPQPCCVPTKLSPLSMLYLDDNSNVVLRLYPNMSVKECGCR}
                                                         105 (SEQ ID NO:301)
      gnl|Pfam|pfam00688, TGFb_propeptide, TGF-beta propeptide. This propeptide is known
as latency associated peptide (LAP) in TGF-beta. LAP is a homodimer which is disulfide
linked to TGF-beta binding protein.
                  CD-Length = 227 residues, 46.3% aligned
                  Score = 48.1 bits (113), Expect = 8e-07
      (SEQ ID NO:302)
      NOV20: 62
                 CPVCVWRQHSRELRLESIKSQILSKLRLKEAPNISREVVKQLLPKAPPLQQILDLHDFQG 121
                       + + | | | ++
                  CRPLDLRRSQKQDRLEAIEGQILSKLGLRRRPRPSKE-----PMVVPEYMLDLYNALS
      Sbjct: 1
      NOV20: 122
                  DALQ--PEDFLEEDEYHATTETVISMAQ----ETDPAVQTDGSPLCCHFHF 166
                       | +|
                                       + +
                                                [+]
                  ELEEGKVGRVPEISDYDGREAGRANTIRSFSHLESDDFEESTPESHRKRFRF 105
      Sbjct: 54
      (SEQ ID NO:303)
```

On page 169, please replace lines 4-11 with the following paragraph:

A disclosed NOV21c polypeptide (SEQ ID NO:68) is 320 amino acid residues in length and is presented using the one-letter amino acid code in Table 21G. The SignalP, Psort and/or Hydropathy results predict that NOV21c has a signal peptide and is likely to be localized to the plasma membrane with a certainty of 0.6000. In alternative embodiments, a NOV21c polypeptide is located to the Golgi body with a certainty of 0.4000, the endoplasmic reticulum (membrane) with a certainty of 0.3000, or the mitochondrial inner membrane with a certainty of

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